									H1122000H		~ ~ 11 11	~ ~ ~ ~	
5.1.4 p5_4578 Compugen Ltd.	n2p model	Search time 45.5 Seconds (without alignments) 5869.482 Million cell updates/sec	caaggcaaagtgttgtctga 1389		50	ters: 566448			Command line parameters: -MODEL=frame+ n2p.model -DEV=xlp -Q=/CGPI2_1/USPTO spool/US09768781/runat_01042003_084730_4952/app_query.fasta_1.1543 -Q=/CGPI2_1/USPTO spool/US09768781/runat_01042003_084730_4952/app_query.fasta_1.1543 -Q=/CGPI2_1/USPTO spool/US09768781-ran2p.rpr_MINMATCH=0.1 -LOOPCH=0 -LOOPEXT=0 -UNITS=EAte -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -USFFQ=US09768781_@CGN 1 1 74 @runat_01042003_084730_4952 -NCPU=6 -ICPU=3 -NO XLEXY -NO MWAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THRRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7	-	results predicted by chance to have a . to the score of the result being printed, of the total score distribution.	Description	MCLeod syndrome-as hypothetical prote hypothetical prote hypothetical prote cytochrome b245 be sopre germination hypothetical prote NADH2 dehydrogenas hypothetical prote NADH2 dehydrogenas hypothetical prote NADH2 dehydrogenas hypothetical prote NADH2 dehydrogenas NADH2 dehydrogenas
GenCore version ight (c) 1993 - 2003	using frame_pl	1, 2003, 08:50:46 ; Se (w 58	- 09-768-781-2 43 atgaacacaagaccacaaca	10.0 , Xgapext 0.5 10.0 , Ygapext 0.5 6.0 , Fgapext 7.0 6.0 , Delext 7.0	segs, 96134422 residues	satisfying chosen parameters	200000000	Match 0% Match 100% first 45 summaries	-DEV=xlp S09F68781/runat_01042 -SUFFIX=n2p.rpr -MINM DD=-1 -MATRIX=blosum62 H=pct -THR MAX=100 -TH EAPSIZE=50 -MINLEN=0 1 74 evanat_01042003 EQUERY -NGG SCORES=0 S=1 -XGAPOP=10 -XGAPE -DELOP=6 -DELEXT=7	***	io. is the number of results predireater than or equal to the scorderived by analysis of the total	SUMMARIES	444 2 139294 439 2 732470 783 2 86825 382 2 70203 745 2 70203 745 2 70203 506 2 H83831 2143 2 71039 508 2 990567 788 2 717163 459 2 717166 459 2 717166
Copyright	- protein se	April	us core: 25	table: BLOSUM62 Xgapop 1 Ygapop 1 Fgapop Delop	283224	of hits	DB seq length: 0 DB seq length: 2	sessing: Minimum Maximum Listing	ine parameters: -ame+ n2p.model 1/USPTO spool/U 3 -QFMT= Easten te -START=1 -EN i=200 -THR SCORE tto -NORM=ext -H by76871 -GCORE -NO MMAP -LARE -NO MMAP -LA	: PIR_73:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*	. 61 -41	\$ Query Score Match Length	932 131 121:5 4 8 120:5 4 7 120:5 4 7 116:5 4 6 116:5 116:5 117:4 111:2 111:4 110:5 111:4 110:5 111:4 110:5 110:5 111:4 110:5
	OM nucleic		Title: Perfect a Sequence:	Scoring	Searched:	Total number	Minimum I Maximum I	Post-processing	Command 11. MODELefra -O=/CGD2 1 -DB=PIR 73 -UNITS=DIC -OUTFMT=DC -USER=USO9 -NO XLEXY -WARN TIME	Database	Pred. score and i	Result No.	10648668901664

nypochetical related to Si probable trar probable tran probable memb probable memb ferric anguik hypothetical NADH2 dehydre oligopetide ABC transport transmembrane NADH2 dehydre oligopetide ABC transport hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical probable high hypothetical hypothetical conserved hypothange 01-Dec-2 conserved hypothange conserved hypothange oncodes a novel		4 4	30	N (T20895	himotropia and
radiated to Si H98589 F990739 F00bable train H86817 F96819 F00bable train F14138 F1413		4		•		Dypotnetical prote
Probable train probable train probable train H85589 probable train H86417 probable ment grade and grade grade grade and grade and grade grade grade and grade grade grade grade and grade grade grade grade and grade grade grade grade grade grade grade grade and grade grad		٠	S	7	T48829	related to SREBP c
H85589 H64817 H64817 H64817 H64817 H64817 H64817 H64817 H64818 H64817 H64817 H64817 H7481 H7481 H71181 H711		4	741	~	F90739	probable transport
H64817 H64817 H64817 H64817 H64817 H64817 H64818 H74138 H74138 H74138 H74138 H74138 H74138 H74138 H74138 H74138 H7414 H744 H74		4	741	N	H85589	
## AH0600 ## AH0600 ## AH0600 ## C		4	786	~	H64817	probable membrane
G82280 ferric anguit G82280 ferric anguit C70190 T17144 T1714 T17144 T1714 T17144 T171		4	740	7	AH0600	probable membrane
734138 hypothetical C86874 transport C86874 AEC transport C86874 AEC transport T17181 NADH2 dehydra T17181 NADH2 dehydra T15528 peptide ABC transportide D72059 peptide ABC transportide D72059 peptide ABC transportical T25628 peptide ABC transportical T25628 peptide ABC transportical D86304 hypothetical T19008 hypothetical D86304 hypothetical D86304 hypothetical D86306 hypothetical		4.	341	~	G82880	ferric anguibactin
CEGESTA ARE transport CEGESTA ARC transport D75104 T17181 NADH2 dehydro T17181 NADH2 dehydro CEGESE D72059 T1532 T1533 T1532 T1533 T1532 T1533 T		4.	412	~	T34138	othetical prot
DG68874 Transmembrane Transmem		4.	443	~	C70190	K+ transport prote
177104 transmembrane 177104 MADH2 dehydromenter 177144 MADH2 dehydromenter 177144 MADH2 dehydromenter 175628 peptide ABC thypothetical 175628 probable Math 179008 probable Math 179008 probable high		4.	339	~	C86874	ABC transporter pe
11/181 NADH2 dehydra Gehydra Gebses C86565 C86565 C86565 C86565 C86565 C86565 C86565 C86565 C8666 C86665 C8666 C8666 C86666 C8666 C86666		4.4	503	N (D75104	transmembrane tran
11.1144 NADLY dehydrogenerical by the peptide ABC (11.13.12) hypothetical hypothetical hypothetical hypothetical besides B8304 hypothetical besides B7268 hypothetical b8268 hypothetical b96506 hypothetical hypothetical b96506 hypothetical hypothetical b96506 hypothetical hypothetical besides besides besides besides besides besides besides besides by by bothetical hypothetical hypothetical hypothetical hypothetical hypothetical besides by by bothetical hypothetical besides besides by by bothetical besides besides by by bothetical besides besides by by bothetical besides by by bothetical besides by by bothetical by by by by bothetical by bothetical by by bothetical by bot		3" "	4. 4 V C	7 (T1/181	
ein XK - human ALIGNMENTS ein XK - human brane transport protein evision 16-Feb-1996 #text_change 01-Dec-2 for McLeod syndrome that encodes a novel		4	4 4 4 4	N C	TI/144	NADH2 dehydrogenas
T15322 T15322 Hypothetical G90476 T25628 Hypothetical D6304 D6304 T19008 S63658 T19008 T19008		r 4	493	4 (072059	origopeptide perme
T25628 hypotherical Na+(290476 Na+(201476 Na+(201476 Na+(201476 Na)) T1381 NADH2 dehydrom NADH2 NA		4	521	1 0	T15322	hypotherical prote
G90476 G90476 T13881 NADH2 dehydrc S65658 D86304 D86304 D86306 T190026 Hypothetical B72688		4	378	8	T25628	hypothetical prote
113881 NADH2 dehydro Sesses NADH2 dehydro Besses hypochetical brooks hypochetical by Conserved hypochetical by Conserved hypothetical hypochetical hypochetical hypothetical h		4	599	n	G90476	_
S63658 NADH2 dehydro 100026 T19008		4	460	N	T13881	dehydroger
D86304 hypothetical T100026 hypothetical T10008 hypothetical B72688 hypothetical B72688 hypothetical S3606 hypothetical S02157 H+-transportical H84685 hypothetical H84685 hypothetical T1GNMENTS ALIGNMENTS ALIGNMENTS ALIGNMENTS ALIGNMENTS		4	474	7	563658	NADH2 dehydrogenas
T100026 brain-specifi B72688 probable high B7368 probable high B7368 probable data B7368 probable vacu C69309 conserved hypothetical B7369 probable vacu C69309 conserved hypothetical B7369 probable high B7369 probable hi		4,	570	~	D86304	hypothetical prote
T19008 Probable high D95506 S37608 S37608 S37608 Probable high Probable high B83808 H84685 C69309 C69309 ALIGNMENTS ein XK - human brane transport protein evision 16-Feb-1996 #text_change 01-Dec-2 .; Danek, A.; Crocker, P.; Monaco, A.P. for McLeod syndrome that encodes a novel D:94273191; PMID:8004674		4	1584	~	T00026	brain-specific ang
B72688 probable high D95506 hypothetical S37608 NADH2 dehydrct S02157 H+-transporti B83808 probable vacu C69309 conserved hyp ALIGNMENTS ein XK - human brane transport protein evision 16-Feb-1996 #text_change 01-Dec-2 .; Danek, A.; Crocker, P.; Monaco, A.P. for McLeod syndrome that encodes a novel D:94273191; PMID:8004674		4	346	7	T19008	hypothetical prote
D96506 D96506 NADD2 dehydrcal S02157 B83808 B4-transportical H84685 C69309 ALIGNMENTS ein XK - human brane transport protein evision 16-Feb-1996 #text_change 01-Dec-2 for McLeod syndrome that encodes a novel D:94273191; PMID:8004674		4	354	~	B72688	probable high-affi
S37608 S37608 S37608 S02157 H+-transport B83808 H84685 C69309 C69309 ALIGNMENTS ein XK - human brane transport protein evision 16-Feb-1996 #text_change 01-Dec-2 for McLeod syndrome that encodes a novel D:94273191; PMID:8004674		4	379	7	D96506	hypothetical prote
S02157 B03808 B03808 B03808 B05808 C69309 C69309 ALIGNMENTS ALIGNMENTS ein XK - human brane transport protein evision 16-Feb-1996 #text_change 01-Dec-2 .; Danek, A.; Crocker, P.; Monaco, A.P. for McLeod syndrome that encodes a novel D:94273191; PMID:8004674		4	384	~	S37608	NADH2 dehydrogenas
H83808 hypothetical H84685 probable vacu C69309 ALIGNMENTS ein XK - human brane transport protein evision 16-Feb-1996 #text_change 01-Dec-2 i Danek, A.; Crocker, P.; Monaco, A.P. for McLeod syndrome that encodes a novel D:94273191; PMID:8004674	100	4.	264	 (802157	H+-transporting tw
H84685 probable vacue C69309 ALIGNMENTS ein XK - human brane transport protein evision 16-Feb-1996 #text_change 01-Dec-2 .; Danek, A.; Crocker, P.; Monaco, A.P. for McLeod syndrome that encodes a novel D:94273191; PMID:8004674	007	4.	358	N (B83808	hypothetical prote
ALIGNMENTS ein XK - human brane transport protein evision 16-Feb-1996 #text_change 01-Dec-2 .; Danek, A.; Crocker, P.; Monaco, A.P. for McLeod syndrome that encodes a novel D:94273191; PMID:8004674	7		780	7 (H84685	` 1
ALIGNMENTS ein XK - human brane transport protein evision 16-Feb-1996 #text_change 01-Dec-2 .; Danek, A.; Crocker, P.; Monaco, A.P. for McLeod syndrome that encodes a novel D:94273191; PMID:8004674	4	'n	2	4	605690	conserved hypothet
ein XK - human brane transport protein evision 16-Feb-1996 #text_change 01-Dec-2 .; Danek, A.; Crocker, P.; Monaco, A.P. for McLeod syndrome that encodes a novel D:94273191; PMID:8004674					ALIGNMENTS	
brane transport protein evision 16-Feb-1996 #text_change 01-Dec-2 .; Danek, A.; Crocker, P.; Monaco, A.P. for McLeod syndrome that encodes a novel D:94273191; PMID:8004674						
ein XK - human brane transport protein evision 16-Feb-1996 #text_change 01-Dec-2 .; Danek, A.; Crocker, P.; Monaco, A.P. for McLeod syndrome that encodes a novel D:94273191; PMID:8004674						
Drane transport protein evision 16-Feb-1996 #text_change 01-Dec-2 .; Danek, A.; Crocker, P.; Monaco, A.P. for McLeod syndrome that encodes a novel D:94273191; PMID:8004674	McLeod syndrom	е-аввосів	ted pr	otei	- human	
evision 16-Feb-1996 #text_change 01-Dec-2 .; Danek, A.; Crocker, P.; Monaco, A.P. for McLeod syndrome that encodes a novel D:94273191; PMID:8004674	N;Alternate na	mes: pro	able me	GE C	transport	
.; Danek, A.; Crocker, P.; Monaco, A.P. for McLeod syndrome that encodes a novel D:94273191; PMID:8004674	C;Species: Hom C:Date: 16-Feb	o sapiene -1996 #86	(man)	,		abusha
.; Danek, A.; Crocker, P.; Monaco, A.P. for McLeod syndrome that encodes a novel D:94273191; PMID:8004674	C; Accession: I	39294: 86	9126	•		26:15:1
for McLeod syndrome that encodes a novel D:94273191, PMID:8004674	R, Ho, M., Chel	ly, J.; C	arter,	ż	Danek, A.; Crocker,	.; Monaco,
tor McLeod syndrome that encodes a novel D:94273191; PMID:8004674	Cell 77, 869-8	80, 1994		١		
A;Accession: I39294 A;Status: preliminarry A;Molecule type: mRNA A;Residues: 1-444 <res></res>	A;Reference nu	אָנָ ע	300 yen	֓֞֜֝֓֓֞֜֜֝֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֡֓֓֡֓֓֓֓֡֓֓	r McLeod Syndrome that 94273191: DMTD:8004674	encodes a
A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-444 <res></res>	A; Accession: I	1				•
A,Molecule type: mRNA A,Residues: 1-444 <res></res>	A;Status: prel	iminary				
A;Residues: 1-444 <res></res>	A, Molecule typ	e: mRNA				
	A,Residues: 1-	444 <res></res>				
A; Cross-references: EMBL: Z32684; NID: q515872; PID: q515873	A;Cross-refere	nces: EME	3L: Z326	34;	NID:g515872; PID:g515873	873

R;Khamlichi, S.; Bailly, P.; Blanchard, D.; Goossens, D.; Cartron, J.P.; Bertrand, O.

Bur. J. Blochem. 228, 931-934, 1995

A.Title: Purification and partial characterization of the erythrocyte Kx protein deficier
A;Reference number: S69126; MuID:95255304; PMID:7737196
A;Accession: S69126
A;Status: preliminary
A;Molecule type: protein
A;Residues: 7-22 <KHA>
C;Genetics:
A;Genetics: A;Genetics: GDB:120499; OMIM:314850
A;Gene: GDB:
A;Cross-references: GDB:12-Xp21.1
C;Keywords: phosphoprotein; transmembrane protein transpor 444 1179 80 110 4 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 3.05e-80 932.00 64.43% 44.53% 36.65% Alignment Scores:
Score:
Score:
Score:
Score:
Score:
Similarity:
Guery Match:
Similarity:
3
DB:

N

ઠે g ઠે 셤 ઠે 요 ઠે 요 8 8 ò

```
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                   원
                                                                                         ð
                                                                                                                        g
                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1153 GTGAAAGTGTTACTGAATTACTGTCATTCCTTGATTGCCTTGCAGCTCATTATTGCTTAT 1212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    973 CTGATITCAGTCACCATCCTCTATGCTGGCATCAACTTCTCTTGCTGGTCAGCTTTGCAG 1032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1033 TTGAGGTTGGCAGACAGAGATCTCGTCGACAAAGGGCAGAACTGGGGACATATGGGCCTG 1092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1093 CACTATAGTGTGAGGTTGGTAGAGAATGTGATCATGGTCTTGGTTTTTTAAGTTCTTTGGA 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        280 LeuCysPheLeuThrLeuLeuTyrThrGly1leAsnMetPheCysTrpSerAlaValGln 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           435
                                                                                                                                                                                                                                                                                                                                                                                                             612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 IlelleLeulleAsnPhePheSerPhePheLeuTyrProTrp1leLeuPheTrpCysSer 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  260 GlyserprophebroGluAsnileGluLysAlaLeuSerArgValGlyThrThrIleVal 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 320 TyrTyrMet1leArgPhe1leGluAsnAla1leLeuLeuLeuLeuTrpTyrLeuPheLys 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    340 ThraspileTyrMetTyrValCysAlaProLeuLeuValLeuGlnLeuLeulleGlyTyr 359
                                                                                                                                                                             315
                                                                                                                                                                                                                                                GCCAAAGATAAACCGCTATCATTATTTATCCATCTAATCCTCTTGGGACCTGTTATCAGA 375
                                                                                                                                                                                                                                                                                                                                                                                           492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGGAGGTGGGCCACTCCATCCGGACCCTGGCTATGCACCGCAATGCCTACAAACGTATG 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GICACCIATGGGGCCACCCITIGCAATATGTTGGCTATCCAGATCAAGTACGATGACTAC 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                733 AAGATTCGCCTTGGGCCACTAGAAGTCCTCTGCATCACCATCTGGCGGACATTGGAGATC 792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      793 ACTICCCGCCTCCTGATICTGGTGCTCTTCTCAGCCACTTTGAAATTGAAGGCTGTGCCC 852
                                                                                                         196 TACATGGTTAGAATCTATCGAAAGAATAGTGAAACTTACTGGATGACATACACCTTTTCT 255
                                      TTTCCATTTAGCATCCTTTTCTCCCACCTTTTTGTACTGTGGGGAGGCTGCATCTGCTTTG 195
                                                                                                                                                                             TTCTTTATGTTTTCATCCATTATGGTCCAGTTGACCCTCATTTTTGTCCACAGAGATCTA 315
                                                                                                                                                                                                                                                                    66
                                                                                                                                          23 SerLeuSerSerThrTyrArgSerGlyGlyAspArgMetTrpGlnAlaLeuThrLeuLeu 42
                                                                                                                                                                                                                                                                                                                                            TATGTCAGCCTCACCCGAAAGAAG----ATGCTAATAGATGGCGAGGAGGTGCTGATAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCACAGATCCAAGCCTTCCTGGGCTCAGTGCCCCAGCTGACCTATCAGCTCTATGTGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGATCTCTGCAGAGGTTCCCCTGGGTAGAGTTGTGCTAATGGTATTTTCCCTGGTATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      200 GluValLy6ValAsnArgLeuAlaTyrValCysIlePheLeuTrpArgSerPheGluIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           853 TICCTAGIGCICAACTICCIGAICAICCICTITIGAGCCCTGGAITAAGTICTGGAGAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                913 GGTGCCCAGATGCCCAATAACATTGAGAAAAACTTCAGCCGGGTCGGCACTCTGGTGGTC
                                                                                                                                                                                                                                                                                                                    US-09-768-781-2 (1-1389) x I39294 (1-444)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                493
                                                                                                                                                                                                                                                                                                                      376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               673
                                                                                                                                                                             256
                                                                                                                                                                                                                43
                                                                                                                                                                                                                                                                                 63
                                                                                                                                                                                                                                                                                                                                                        83
                                                                                                                                                                                                                                                                                                                                                                                           436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    553
```

요

유 ò g

8

셤

ò

유 ò 셤

ሯ

셤 ò

8

유

ઠ 요 ઠે 유 ઠે 셤 ò

셤 ò

```
A;Accession: T32470
A;Atatus: preliminary; translated from GB/EMBL/DDBJ
A;Atatus: preliminary; bNA
A;Residues: 1-439 <FUL>
A;Residues: 1-439 <FUL>
A;Cross-references: EMBL:AF026213; PIDN:AAB71305.1; GSPDB:GN00028; CESP:F08F1.5
A;Experimental source: strain Bristol N2; clone F08F1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 04-Mar-2000
C;Accession: T32470
R;Fulton, B: aubmitted to the EMBL Data Library, September 1997
A;Description: The sequence of C. elegans cosmid F08F1.
1213 CTGATTTCCATTGGCTTCATGCTCCTTTTCTTCCAGTACTTGCATCCATTGCGATGCGCTCACTC 1272
                                                                                                         ITCACCCATAATGTAGTAGAC-----TACCTCCATTGTGTCTGC-----TGT 1314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      591
                               360 CysThrAlaIleLeuPheMetLeuValPheTyrGlnPhePheHisProCysLysLysLeu 379
                                                                                                                                           |||::: :::||| ::: ||| 380 PheSerSerSerValSerGluGlyPheGlnArgTrpLeuArgCysPheCysTrpAlaCys 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    328 CCGCTATCATTATTATGCATCTAATCCTC----TTGGGACCTGTTATCAGATGTTTG 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :::|||:::
146 LysAlaLeuTyr---TyrGlyTrpMetPheArgLysSerSerAsnGluAsn------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                382 GAGGCCATGATTAAGTACCTCACACTGTGGAAGAAAAAGAGGAGGAGGAGGAGCCCTATGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGCCTCACCCGAAAGAAGATGCTAATAGATGGCGAGGAGGTGCTGATAGAATGGGAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCCACTCCATCCGGACCCTGGCTATGCACCGCAATGCCTACAAACGTATGTCACAG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   197 IleIleGlnGlySerIleAlaAlaSerTyrPheGlnAsnTyrTyrGlnThrGlyThrTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCTATCAGCTCTATGTGAGCCTGATCTCTGCAGAGGTTCCCCTGGGTAGAGTTGTGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----ThrAspGlyGluLys-------ThrAspGlyGluLys-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: X
A;Introns: 20/1; 72/3; 137/3; 184/2; 263/3; 289/3; 339/3; 369/1
C;Superfamily: Caenorhabditis elegans hypothetical protein F08F1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein F08F1.5 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-768-781-2 (1-1389) x T32470 (1-439)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.000618
131.00
37.39%
19.42%
5.15%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                     1315 CACCAG 1320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Gene: CESP: F08F1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
```

Percent Similarity: 34.58* Conservative: 68 Best Local Similarity: 19.60* Mismatches: 166 Query Match: 4.78* Indels: 131 DB: 2 Gaps: 19 US-09-768-781-2 (1-1389) x A96825 (1-783)	256 TTCTTTATGTTTTCATCCATTATGGTCCAGTTGACCCTCATTTTTGTCCACAGAGATCTA 31	316	352 ATCCTCTTGGGACCTGTTATCAGATGTTTGGAGCCATGATTAAGTACCTCACACTGTGG 411	412 AAGAAAGAGGAGGAGGAGCCCTATGTCAGCCTCACCCGAAAGAAGATGCTA 465	466 ATAGATGGCGAGGAGGTGCTGATAGAATGGGAGGTGGGCCACTCCATCCGGACCCTGGCT 525 ::	526 ATGCACCGCAATGCCTACAAACGTATGTCACAGATCCAAGCCTTCCTG 573	574 GGCTCAGTGCCCCAGCTGACCTATGTGAGCCTGATCTCTGCAGAGGTTCCC 633	634 CTGGGTAGAGTTGTGCTAATGGTATTTCCCTGGTATCTGTCACCTATGGGGCCACCCTT 69 11	694 IGCAATATGTTGGCTATCCAGATCAAGTACGATGACTACAAGATTCGCCTT 74.	745 GGGCCACTAGAAGTCCTCTGCATCACCATCTGGCGGACATTGGAGATCACTTCCCGCCTC	805 199	865 AACTICCTGAICCTCTTGAGCCCTGGATTAAGTICTGGAGAAGT	219 inrval 913 GGTGCC	234ProLysArgAsnProLysGluLysTyrLeuSerLysAlaGluThrLeuValPhe 2	973 CTGATTTCAGTC 984	985 ACCATCCTCTAIGCTGGCATCAACTTCTCTTGCTGGTCAGCTTTGCAGTTGAGGTTGGCA 104- 11:1::	1045 GACAGAGATCTCGTCGACAAA	1075
Pee Quy DB	yo da	<i>&</i> 8	<i>ò</i> €	<i>ò</i> €	& 8 	<i>γ</i> ο 49	<i>장</i> 옵	λο α -	δ dd	ò 4		onso, , K.; Qy	ali, C. Oy		<i>장</i> 옵	<i>д</i>	ò á	8 <i>6</i>
Oy 652 ATGGTATTTTCCCTGGTATCTGTCACCTATGGGGCCACCCTTTGCAATATGTTGGCTATC 711 Db 227 LeuLeuLeuSerIleIsSerIleSerTrpSerValValValGlnAsnargSerLeuArg 246 Oy 712 CAGATCAAGTACGAAGATTCGCCTTGGGCCACTAGAAGTCCTCTGCATCACC 771 Db 247 Marilaard Agarta Caracaagatt 10			ACTTCAGC :::	CATCAACTTC	AAGGGCAG	1072 AACTGGGGACATATGGGCCTGCACTATAGTGTGAGG 324 ArgTrpArtytleuThrAlaltytSerValGlu	TTCCTTGATTGCC	1192 TIGCAGCTCATTATTGCTTATCGATTTCCATTGGCTTCATCCTTTTCT 1193 TIGCAGCTCATTATTGCTTATCTATTGCTTTCTTCTT 110	1252 TTGCATCCATTGCGC 1266	DD 350 FIRETSFIOABINIG 384 RESULT 3 A96825	hypothetical protein T8K14.18 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: A96825	e, O.; Al 1.; Dewar	ı, E.; Kim R.; Marzi	A. A. L. M.	A;1ttle: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719; PMID:11130712 A;Accession: A96825	A,Nolecule type: DNA A,Nolecule type: DNA A,Residues: 1-783 <sto> A,Cross_references: GB:AE005173; NID:g4835769; PIDN:AAD30236.1; GSPDB:GN00141</sto>	Cjemetics: A;Gene: T8K14.18 A;Map position: 1	Alignment Scores: 0.00552 Length: 783 Pred. No.: 121.50 Matches: 89

us-09-768-781-2.n2p.rpr

Db 307 PheGlyTyrIleGlyPheArgPheSerIleIleAlaLeuThrLysArgPheTyrLeuGly 326	Db 104 LeuAsnGlyLeu	LeuAsnGlyLeuLeuAsnGlyIleSerTrpProIleAlaGlnPheAlaIleAlaSerAla 123
Qy 1108 TTGGTAGAAATGTGATCATGGTCTTGGTTTTTAAGTTCTTTGGAGTG 1155	Qy 526 ATGCACCGCAAT	526 ATGCACCGCAATGCCTACAAACGTATGACACAGATCCAAGCCTTCTGGGGTCAGTGCCC 585
:::	 Db 124 SerProAspAsn	
Qy 1155 1155	586	CAGCIGACCIATCAGCICTAIGIGAGCCIGAICTCTGCAGAGGTICCCCTGGGTAGAGTT 645
Db 347 MetTyrLeuLys1leProLysLysTyrTrpLeuPheLeuProThrIleLeuSerValLys 366	Db 144 ServallleGly.	AsnTyrValTyrAlaGlnMetAlaGluLeuThrLeuLysGluGln 162
Oy 1156	Oy 646 GTGCTAATGGTA ::::: Db 163 MetMet	GTGCTAATGGTATTTCCCTGGTATCTGTCACCTATGGGGCCACCCTTTGCAATATGTTG 705 ::::::
Qy 1174TGTCATTCCTTGATTGCCTTGCGAGCTCATTATTGCTTATCGATTTCCATTGGCTTC 1230	Qy 706 GCT Db 179 LeuAlaTyrTyr	GCTATCCAGATCAAGATACAAGATTCGCCTTGGCCACTAGAA 756 LeualaTyrTyrLeuLeuPheAsnTyrValThrProLysArgLysGlyGlyAsnValGlu 198
Qy 1231 ATGCTCCTTTTCTTCCAGTACTTGCATCCATTGCGCTCACTC 1272	Oy 757 GTCCTCTGCATC ::: Db 199 GluLeuHisLeu	GTCCTCTGCATCACCATCTGGGGACATTGGAGATCACTTCCCGCCTCCTGATTCTGGTG 816
Qy 1273 TTCACCCATAATGTAGTAGCTCCCATTGTGTCTGCTGT 1314	Qy 817 CTCTTCTCAGCC Db 219 AlaPheAlaSerGl	CTCTTCTCAGCC
RESULT 4 E75203 hvpothetical protein PAB2250 - Pvrococcus abvssi (strain Orsav)	Oy 829ACTTTG Db 239 GlyThrThrAla	ACTITGAAATIGAAGGCTGTGCCCTTCCTAGTGCTCAACTTCCTGATCATCCTC 882
C;Species: Pyrococcus abyssi C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999 C;Accession: E75203		TTTGAGCCCTGGATTAAGTTCTGGAGAGAGTGGCCCAGATGCCCAATAACATTGAGAAA 942 :::::::: ::: SerTvrVallthaseTtrDhrqAlaAsDValGlvLv8ValArgGluMetValSer 273
submitted to the EMBL Data Library, July 1999 A.Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru A.Reference number: A75001 A.Accession: E75203	943 A 274 L	943 AACTTCAGCGGGTCGGCACTCTGGTGGTCCTGATTTCAGTCACC 987
A;Status: preliminary A;Molecule type: DDS A;Rebidues: 1-322 < KKW> A;Cross-references: GB:AJ248283; GB:AL096836; NID:g5457433; PIDN:CAB49076.1; PID:e151497	Qy 988 ATCTCTATGCT ::: ::: Db 294 ValPheLeu	ATCCTCTATGCTGGCATCACTTCTCTTGCTGGTTTGCAGTTGAGGTTGGCA 1044 ::: ::::
A;Experimental source: strain Orsay C;Genetics: A;Gene: PAB2250	Oy 1045 GACAGAGATCTC ::: Db 313 ArglveValleu	GACAGAGATCTCGTCGACAAAGGGCAGAACTGGGGACATATGGGCCTGCACTATAGTGTG 1104 ::: ArgivsValleuValAlaTvrArgArgSerSerLeuAla1leG1vG1yLeu 329
Alignment Scores: Pred. No.: Score: Score: Percent Similarity: Best Local Similarity: Alignatches: Alignatc	1105	349
4.74% Indels: 2 Gaps:	Qy 1165 CTGAATTACTGT Db 350 LeuGlyGluLeu	.165 CTGAATTACTGTCATTCCTTGATTGCCTTGCAGCTCATTATTGCTTATCTGATTTCCATT 1224
US-09-768-781-2 (1-1389) x E75203 (1-382) Qy 253 ICTICITIAIGTITICAICCATTAIGGICCAGTIGACCCTCATTITICIC 303	Qy . 1225 GGCTTCATGCTCCTT 1239 Db 370 SerIleAlaLeuile 374	CTT 1239 ::: Ile 374
304 CACAGAGATCTAGCCAAGATAAACCGCTATCATTATTATGCATCTAATCCTCTTGGGA	RESULT 5 T02024 Cytochrome b245 beta c Cytochrote names: int N'Alternate names: int	hain homolog rbohA - rice (fragment) rinsic plasma membrane protein RbohAOsp
Qy 364 CCTGTTATCAGATGTTTGGAGGCCATGATTAAGTACCTCACACTGTGGAAGAAGAGGAG 423	; Date: 26-Feb-1999 #s; Accession: T02024; Keller, T.; Damude,	C,Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 23-Jul-1999 C;Accession: T02024 #sequence_revision 26-Feb-1999 #text_change 23-Jul-1999 R;Acler, T.; Damude, H.G.; Werner, D.; Doerner, P.; Dixon, R.A.; Lamb, C. whattered to the Empt. Data Tibrary July 1997
Oy 424 CAGGAGGAGCCTATGTCAGCCTCACCGAAAGAAGATGCTAATAGATGGGAGGAGGAGGAGGAGGAGGAGGAGAGAGA	pescription: A plant, Reference number: Z1	Date initially card report NADPH oxidase gp91phox subunit gene end 4499
Oy 484 CTGATAGAATGGGAGGTGGGCCACTCCATCCGGACCTGGCT 525	;Status: translated f ;Molecule type: mRNA ;Residues: 1-745 <kel< td=""><td>rom GB/EMBL/DDBJ</td></kel<>	rom GB/EMBL/DDBJ

```
952 CGGGTCGCCACTCTGGTGGTCCTGATTTCAGTCACCATCCTCTATGCTGGCATCAACTTC 1011
                                                                                                                                                                                                                                      GATCTAGCCAAAGATAAACCGCTATCATTATTATGCATCTAATCCTCTTGGGACCTGTT 369
                                                                                                                                                                                                                                                                                                 370 ATCAGATGTTTGGAGGCCATGATTAAGTACCTC---------ACA 405
                                                                                                                                                                                                                                                                                                                                                                                       154 SerGlnAsnLeuAlaGlyLeuArglysLysSerSerIleArgLysileSer----- 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      631 CCCTGGGTAGAGTTGTGCTAATGGTATTTTCCCTGGTATCTGTCACCTATGGGGCCCACC 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  691 CITTGCAATATGTTGGCTATCCAGATCAAGTACGATGACTACAAGATTCGCCTTGGGCCA 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           206 ArgAsnArgTyrValPheAspValMetGlyTyrCysValThrThrAlaLysGlyAlaAla 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1012 TCTTGCTGGTCAGCTTTGCAGTTGAGGTTGGCAGACAGAGATCTCGTCGACAAAGGGCAG 1071
                                                                                                                                                                                                                                                                                                                                                                CTGTGGAAGAAAAAGAGGAGCAGGAGGCCCTATGTCAGCCTCACCCGAAAGAAGATGCTA 465
                                                                                                                                                                                                                                                                                                                                                                                                                              166 ATAGATGGCGAGGAGGTGCTGATAGAATGGGAGGTGGGCCACTCCATCCGGACCCTGGCT 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            526 AIGCACCGCAAIGCCIACAAACGIAIGICACAGAIC-------CAAGCCIIC 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          571 CTGGGCTCAGTGCCCCAGCTGACCTATCAGCTCTATGTGAGCCTGATCTCTGCAGAGGTT 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       793 ACTICCCGCCTCCTGAITCTGGTGCTC---TICTCAGCCACTITGAAATTGAAGGCTGTG 849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187 Leu---AlaLeuTrpileGlyileMetAlaGlyLeuPheThrTrpLysPheMetGlnTyr 205
                                                                                                                                                                                                                                                                         77
                                                                                                                                                                                                                                                                                                                    |||| ||||||| :::|||| :::
78 GlyArgIleThrGluAlaGluValLysGluIleIleMetLeuSerAlaSerAlaAsnLys 97
                                                                                                                                                                                                                                                                58 AspAsnSerPheAspSerArgLeuGlnIlePhePheGluMetValAspLysAsnAlaAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----TGGCGGACATTGGAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         892 TGGATTAAGTTCTGGAGAAGTGGTGCCCAGATGCCCAATAACATTGAGAAAAACTTCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     171 -----ThrserLeuserTyr-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: EMBL: AF015302; NID: 92654869; PID: 92654870
                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
                             A,Gene: rbohA
C,Keywords: calcium binding; membrane protein
                                                                                                                                                                              Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   751 CTAGAAGTCCTCTGCATCACCATC-----
                                                                                                                                                                                                        US-09-768-781-2 (1-1389) x T02024 (1-745)
                                                                                         0.00681
120.50
36.44%
20.74%
                                                                                                                         Percent Similarity:
Best Local Similarity:
                                                                            Alignment Scores:
Pred. No.:
                                                                                                                                                          Query Match:
                 Genetics
                                                                                                                                                                                                                                     310
                                                                                                                                                                                                                                                                                                                                                                900
                                                                                                                                                                                                                                                                                                                                                                                               98
                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                              셞
                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                   ሯ
                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                          윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ሯ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 유
```

```
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and c
A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:AP001512; GB:BA000004; NID:g10174030; PIDN:BAB05175.1; GSPDB:GN001
A;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                     sopre germination protein BH1456 [imported] - Bacillus halodurans (strain C-125)
C.Species: Bacillus halodurans
C.Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
                                                                                                              |||||||||||:::
325 GlyValileMetValValCysMetIleIleAlaPheThrLeuAlaThrArgTrpPheArg 344
                                                                                                                                            345 ArgSerLeuValLysLeuProArgProPheAspLysLeuThrGlyPheAsnAlaPheTrp 364
                                                                                                                                                                                                                      365 ---TyrSerHisHisLeuPhellelleValTyrIleAlaLeuIleValHisGlyGluCys 383
305 TyrPheGlyGluIleLysProThrTyrPheThrLeuValLysGlyValGluGlyIleThr 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||| :::|||| :::||| 34 GlnSerSerAspPheThrGlnPheThrMetAspAlalleGlnLeuArgTyrHisLeuPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98 AGGAAGATGTCATCCGTGGAGCCAACC------CCCGATTTACTTTTCCATTTAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 LysSerLysAlaLeuThrLeuHisGluLeuLysArgGluLeuPro-----IleAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           281 ICCAGITGACCCICATITITGI --- CCACAGAGAICTAGCCAAAGAIAAACCGCIAICAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAATGGACAGAGTTTATGAAATTCCTGAGGAGCCAAATGTGGATCCGGTTTCATCTCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SerileHisileValGlnAsnAspLysGluLeuAsnThrTyrLeu-------
                                                                                                                                                                                    1168 AATTACTGTCATTCCTTG-----ATTGCCTTGCAGCTCATTATT----
                                                                                                                                                                                                                                                           1207 GCTTATCTGATTTCCATTGGCTTCATGCTCCTTTTCTTCCAGTACTTG 1254
                                                                                                                                                                                                                                                                                   506
103
82
163
157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C. Superfamily: spore germination protein gerBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-768-781-2 (1-1389) x H83831 (1-506)
                                      1117 AATGIGATCAIGGICTTGGTTTT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.0153
116.50
36.63%
20.40%
4.58%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1-506 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                              Accession: H83831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Accession: H83831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: BH1456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91
                                    ò
                                                                        셤
                                                                                                            à
                                                                                                                                          g
                                                                                                                                                                                  ò
                                                                                                                                                                                                                     유
                                                                                                                                                                                                                                                                                             원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

338 TA---TTTATGCATCTAATCCTCTTGGGACCTGTTATCAGATGTTTGGAGGCCATGATTA 394

1 09:03:24 2003

Tue Apr

 	41		lleLeu 188	CTGGCTATGCACCGC- 534 ::: ::: Valvalardandrgi 206			ATCTCTG 622	ProAspArgValAlas 246			GACTACAAGATTCGCC 742 :::::: benTvrDheI.enI.veT 284			ArgLeuPheSerValL 299		TyrHisProGluLeuI 319	GTGCCCTTCCTAG 859	ileProPheProProi 339	TGGAGAAGTGGTG 916	LeuArgGluAlaGlyA 357	ACTCTGGTG 969 :: GlyllevallleGlyT 377	-GTCCTGATTTCAGTCACCATCCTCTATG 997	::: 	GCAGACAGATCTCG 1057	403	GTGAGGTTGGTAGAGA 1117	 ProValTyrArgMetGlyA 410	TTACTGAATTACTGTC 1177	 LeuAlaAlaGlnLeuT 426	ATTGGCTTCATGCTCC 1237	
:: :: :: :: :: :: :: :: :: :: :: :: ::	AraAraLeuPr	AAGAGGAGGAGGCCCTATGTCAGCCTCACGAAAGAAGATGCTAATAGATGGGG	ledludluTyrdluValGlySerLeuSerHisThrArgValAlaileLeu	AGGAGGTGATAGAATGGGAGGTGGGCCACTCCATCCGACCCTGGCTATGCACGC- 	AATGCCTACAAACGTATGTCACAGATCCAAGCCTTCCTGGGCT		CAGTGCCCCAGCTGACCTATGAGCCTG	spserSerGlnSerProPheProLeuLleAspThrGluArgProAspArgValAlaS	CAGAGGTTCCCCTGGGTAGAGTTGTGCTAATGGTATTTTCCCTGGTATCTGTCACCTATG	erValLeuAlaGluGlyLysValCysValLeuThrAspGlySerProSerAlaIleThrG	GGGCCCCTTTGCAATATGTTGGCTATCCAGATCAAGTACGATGACTACAAGATTGGC 	iii beuvalgiuriieriiesei seriyi gim	TTGGGCCACTAGAAGTCCTCTGCATCACCATCTGGGCGACATTGGAGATCACTTCCCGCC	IleAlaSerIlePheArgLeuIle		euPheSerIlePheValThrProMetTyrValAlaValLeuThrTyrHisProGluLeuI	-GTGCTCTTCTCAGCCACTTTGAAATTGAAGGCTGTGCCCTTCCTAG	leProGlnAspLeuLeuAlaThrLeuThrLeuSerArgSerAlaIleProPheProProI	TGCTCAACTICCTGAICAICCTCTTTGAGCCCTGGAITAAGTICTGGAGAAGTGGTG	leLeuGluAlaLeuPheLeuGluValThrileGluLeuLeuArgGluAlaGlyA	CCCAGATGCCCAATAACATTGAGAAAACTTCAGCCGGGTCGGCACTCTGGTG -::::	GTCCTGATTTCAK	::: :::	CTGGCATCAACTTCTTGCTGGTCAGCTTTGCAGTTGAGGTTGGCAGACAGA	ThrThr	TCGACAAAGGGCAGAACTGGGGACATATGGGCCTGCACTATAGTGTGAGGTTGGTAGA	Proj	ATGTGATCATGGTCTTGGTTTTTAAGTTCTTTGGAGTGAAAGTGTTACTGAATTACTGTC		ATTCCTTGATTGCCTTGCAGCTCATTATTGCTTATCTGATTTCCATTGGCTTCATGCTCC	
				AGGAGGT		leAsnAspIleAsp				-	-			rpHis	-									_	7 laLeuAlaSerPheThrThr						
Db 136			Db 172	Oy 476				Db 226		Db 246	Qy 683			Db 284		Dp 299	Qy 814	Db 319	Oy 860	339 pp	Oy 917 Db 357	Oy 970	77E qa	Оу 998	397	Qy 1058	Db 404	Oy 1118	Db 410	Oy 1178	

```
hypotherical protein F7A10.23 [imported] - Arabidopsis thaliana
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C; Accession: G56595
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.; Liu, S.L.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malti, R.; Marziali, Rizzo, M.; Rooney, T.; Kowley, D.; Sakno, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.W.; Sun, H.; Tallon, Ker, M.; W. D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome lof the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712
A; Residues: preliminary
A; Molecule type: DNA
A; Residues: 1-2143 ASTP.
A; Constant Arabidopsis A; Carpo, Astronomerical A; Carpo, A; Carpo, Carponerical A; Carpo, Carponerical A; Carpo, A; Carponerical A; Carpo, Carponerical A; Carponerical 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AE005173; NID:g10645420; PIDN:AAG21537.1; GSPDB:GN00141 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          698 ValValCysSerIleMetAlaPheLeuArgSerLeuGlnValGluMetAlaLeuThr 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SerAlaLysProLeuAspAspLeuLysTyrLysLeuPheSerAlaArgGluAsnAsnVal 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 GTCATCCGTGGAGCCAACCCCCGATTTACTTTTTCCATTTAGCATCCTTTTCTCCACCTTT 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------AAGTACCTCACACTGTGGAAAAAGAGAGCAG--- 426
443 euThrLeuGlnSerLeuGlyArgProPheLeuHisProIleTyrProPheTyrTrpLysA 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |||||||
738 LeuSerPheLeuSerLysSerSerValLeuLeuGlylleSerLeuThrValProLeuMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -------AAACGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         334 TCATTATTATGCATCTAATCCTCTTGGGACCTGTTATCAGATGTTTGGAGGCCATGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166 TIGIACIGIGGGAGGCIGCA--------TCIGCIITGIACAIGGII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   250 TTTTCTTTCTTTTCATCCATTATGGTCCAGTTGACCCTC-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           205 AGAATCTATCGAAAGAATAGTGAAACTTACTGGATGACATACACC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-768-781-2 (1-1389) x G96595 (1-2143)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.0198
116.50
33.68%
20.50%
                                                                         1283 ATGTAGTAGAC 1293
                                                                                                                                           463 spleulysAsp 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
```

~

A;Title: Complete sequence of the mitochondrial DNA of Chlamydomonas eugametos. A;Reference number: 217244; MUID:98145434; PMID:9484440 A;Accession: T11039 A;Actus: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-498 cDEN> A;Cross-references: EMBL:AF008237; NID:92865253; PID:92865257; PIDN:AAC39340.1 C;Genetics: mitochondrion A;Note: mad4 C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4 C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4 C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;	Alignment Scores: Pred. No.: Score: Score: Percent Similarity: Dest Local Similarity: Query Match: 2 Gaps: Alignment Scores: Anterial Scores: Ante	US-09-768-781-2 (1-1389) x T11039 (1-498) QY 592 ACCTATCAGCTTATGTGAGCCTGATCTCTGCAGAGGTTCCCCTGGGTAGAGTTGTGCTA 651 ::: ::: ::: Db 40 ThrTyrCysLeuPheValThrMetVal	OY 652 AIGGIATTITCCCTGGTATCTGTCACCTATGGGGCC	745GGGCCACTAGAAGTCCTCTGCATCACCATCTGGCGGACATTGGAG 7 91 LeuleuThrSerAlaLeuPheProIleCysIleMetValMetArgThrPheLysGlyTyr 1 790 ATCACTTCCGGCTCGATTCTGGTGCTCTTCTCAGCCACTTTGAAATTGAAGGCTGTG 8		Qy 889 CCCTGGATTAAGTTCTGGAGAGTGGCCCCAATAACATTGAAAAATTC 948 Db 148		
Qy 427 GAGGAGCCCTATGTCAGCCTCACCCGAAAGAAGATGCTAATAGATGGCGAGGAGGTGCTG 486 Db 838 ThrSerProflyThrSer	Qy 604 TATGTGAGCCTGATCTCTGCAGAGGTTCCCCTGGGTAGAGTTGTGCTAATGGTATTTTCC 663 Db 875 SerHisSer	Qy 724 GAT	Db 925 ProAlaLeuLeuSerLeuCysCysGlyMetValLysTrpLysAspAspCysTrplleLeu 944 Qy 775 TGGCGGACATTGGAGATCACTTCCCGCCTCCTGATCTGGTGCTCTTCTCAGCCACTTTG 834	965 AlavalileAlavalLysProTrpThrIleGlyValSerPheLeuLeuValLeuPhe 889 CCCTGGATTAAGTTCTGGAGAAGTGGTGCCCAGATGCCCCAATAACATTGAGAAAAACTTC 983	949 AGCCGGGTCGCACTCTGGTGGTCCTGATTTCAGTCACCATCCTCTATGCTGGCATCAAC 100 :::	Db 1000 PheTyrLeuThrArgLysGlnThrSerPheValCysPheLeuAlaLeuLeuGuGlyLeu 1019 Cy 1042 GCAGACAGAGATCTCGTCGACAAAGGGCAGAACTGGGGACAT 1083 Db 1020 AlaAlaPheLeuGlyTrpHisGlnAspLysAlaPheAlaGlyAlaSerValGlyTyr 1039 Cy 1084 ATGGGCCTGCACTATGTGTGAGGTTGGTAGAAATGTG 1122 Db 1040 PheThrPheLeuSerLeuLeuAlaGlyAcAlaLeuAlaValSerSerThrGluLeuVal 1059	1123 ATCATGGTTTTTAAGTTCTTTGGAGTGAAGTGTTACTGAATTACTGTCATTCC 118 1060 LeuproValTyrValTyrAsp	RESULT 8 T11039 NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - Chlamydomonas eugametos mitochor C;Species: mitochondrion Chlamydomonas eugametos C;Species: mitochondrion Chlamydomonas eugametos C;Apate: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 03-Jun-2002 C;Accession: T11039 R;Denovan-Wright, E.M.; Nedelcu, A.M.; Lee, R.W. Plant Mol. Biol. 36, 285-295, 1998

```
SCTTTGCAGTTGAGGTTGGCAGACAGAGATCTCGTCGACAAAGGG 1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGGGCCTGCACTATAGTGTGAGGTTGGTAGAGAATGTGATCATG 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -------GCCTTGCAGCTCATTATTGCTTATT 1218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------ ATCAACTTC----- 1011
                                                                                                                        687
                                                                                                                                                                                                          744
                                                                                                                                                                                                                                                                                        789
                                                                                                                                                                                                                                                                                                                  ||| :::|||||| ::: |||||| :::
LeuPheProlleCyslleMetValMetArgThrPheLysGlyTyr 110
                                                                                                                                                                                                                                                                                                                                                                                                 ||| :::|||::::::
LeuGluIleVallleTyrGlyAlaLeuAsnValLeuAspLeuL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rggagaagtggrgccagatgcccaataacattgagaaaaacttc 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ThrMetGlyGlySerLeulleLeuLeuProllellePheValLeu 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SerThrSerLeulleTyrLeuLeuCysAshPheGlySerGlnHis 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        220
                                        STGAGCCTGATCTCTGCAGAGGTTCCCCTGGGTAGAGTTGTGCTA 651
                                                                                                                                                                                                                                                                                                                                                                          TIGATICTGGTGCTCTTCTCAGCCACTTTGAAATTGAAGGCTGTG 849
                                                                                                                                                                                                                                                                                                                                                                                                                                                            -------CTAGTGCTCAACTTCCTGATCATCCTCTTTGAG 888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------GGCACTCTGGTGGTCCTGATTTCAGTCACCATCCTC 993
                                                                             /alThrMetVal-------ValLeuLeu 51
                                                                                                                                                           Irpserile---TyraspalaileGlyHisSerLeuGlnMetVal 70
                                                                                                                                                                                                                                  CTAGAAGTCCTCTGCATCACCATCTGGCGGACATTGGAG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATCTGTCACCTATGGGGCC-----
                                                                                                                                                                                                          TTGGCTATCCAGATCAAGTACGATGACTACAAGATTCGCCTT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :::.
SerAlaTyrTyrLeuLeuSerGluArgGlnMetIle-----
T11039 (1-498)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
```

:::	472GCGGAGGAGGTGCTGATAGAATGGGAGGTGGGCCACTCCATC 513 218 ValGlualaserSerAspGluIleValGlyLeuIlePheArgGluIleGlyTyrValIle 237 514 CGGACCCTGGCTATGCACCGCAATGCCTACAACGTATGTCAAGATCCAAGCCTTCCTG 573	AlaTyrLeulleLeu1lePheProPhePheSerLeuLeuTyrSer GGCTCAGTGCCCCAGCTGACCThePheProPhePheSerLeuLeuTyrSer GGCTCAGTGCCCCAGCTGACC	GTGAGCCTGATCTCTGCAGAGGTTCCCCTGGGTAGAGTTGTGCTAATGGTATTTCCCTG	295 ValAsnValSerPhe	778 CGGACATTGGAGATCACTTCCCGCCTCCTGATTCTGGTGCTCTTCTCAGCCACTTTGAAA 837 324 ABNAXGLeuLygSerSerIleTyrPheMetPheSerValSerPhe 340 838 TTGAAGGCTGTGCCTTCCTAGTGCTCAACTTCCTGATCATCCTTTTGAGCCCTGG 894	ATTAAGTTCTGGAGAAGTGGTGCCCAGTGCCCATAACATTGAGAAAAACTTCAGCCGG ::: IeserTytasparg	955 GTCGGCACTCTGGTGGTCCTGATTTCAGTCACCATCCTCTATGCTGGCATCAACTTCTT 1014		GTTTTPAGTTCTTTGGAGTGAAAGTGTTACTGAATTACTGTCATTCCTTGATTGCCTTG :::		Oy 1288 GTAGACTAC 1296 Db 473 PheAspTyr 475 RESULT 10
Db 239 ProGluAlaHisValAlaAlaProThrAlaGlySerValLeuLeuAlaGlyValLeuLeu 258 Qy 1219 TCCATTGGCTTCATGCTCCTTTTCTTCCAGTACTTGCATCCATTGCGCTCACCTTCACC 1278 Db 259 LysbeuGlyGlyLeuGlyPhelleArgPhemetileProlleLeuProSerPheThr 277 Db 1279 CATAATGTAGACTACCTCCATTGGTCAC 1311	Db 278 AlaSerIlePheProLeuValCysCysMetCys 288 RESULT 9 D90567	etical protein MYPU 4440 [imported] - Mycoplasma pulmonis (strain UAB CTIP) ies: Mycoplasma pulmonis : 24-May-2001 #Sequence_revision 24-May-2001 #text_change 03-Aug-2001 ssion: D90567 baud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.; c Acids Res. 29, 2145-2153, 2001	SPDB:GN00153		Alignment Scores: Alignment Scores: O.0264 Length: 508 Score: 114.00 Matches: 92 Percent Similarity: 35.59\$ Conservative: 87 Best Local Similarity: 18.29\$ Mismatches: 168 Ouery Match: 2. Gaps:	US-09-768-781-2 (1-1389) x D90567 (1-508) QY 31 ACCTCGACAATGGACAGAGTTTATGAAATTCCTGAGAGCCAAATGTGGATCCGGTTTCA 90 QY 11 ACCTCGACAATGGACAGAGTTTATATAAATTCCTGAGAGCCAAATGTGGATCCGGTTTCA 90 QY 11 ACCTCGACAATGGACAGAGTTATGAAATTCCTGAGAGCCAAATGTCGATCCGGTTTCA 90 QY 11 ACCTCGACAATGAGAGTTATGAAATGTTCCTGAGAGAGCCAAATGTCGATCCGGTTTCA 90 QY 11 ACCTCGACAATGAGAGTTATGAAATGTTCCTGAAATGTCCTGAAATGTATATATA	Qy 91 TCTCTGGAGGAAGATGTCATCCGTGGAGCCAACCCCCGATTTACTTTTCCATTTAGCATC 150 Db	Oy 151 CTTTCTCCACCTTTTTGTACTGGGGGGGGCTGCATCTGTACATGGTT 204	256 TICTITATGITITCATCCATT		390 185 450

Tue Apr

us-09-768-781-2.n2p.rpr

Qy 847 GTGCCCTTCCTAGTGCTCAACTTCCTGATCATCTTTGAGCCCTGGATTAAGTTC 903	333 AsnTyrGluArgThrHisSerArgIleMetLeuLeuSerArgGlyLeuGlnThrLeu 351 1066	0y 1156 AAAGTGTTACTGAATTACTGCTTACTGCAGTTATTGCTTATTGTATG	RESULT 11 A66299 hypothetical protein F309.18 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001 C;Accession. A66299 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H. ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000	hors: Hunte Li, J.H.; M.; Roone hors: Salzb M.; Wu, D.; He: Sequenc ession: A86 tus: prelim ecule type: ludes: 1-78 ss referenc etics:	Alignment Scores: Alignment Scores: Pred. No.: Score: 111.50 Marches: 89 Percent Similarity: 136.27\$ Conservative: Best Local Similarity: 4.38\$ Indels: Caps: 2 Gaps:	US-09-768-781-2 (1-1389) x A86299 (1-785) Qy 148 ATCCTTTTCTCCACCTTTTTGTACTGTGGGGAGGCTGCATCT 189
NADH2 dehydrogenase (ubiquinone) (BC 1.6.5.3) chain 4 [similarity] - Pygathrix bieti C;Species: mitochondrion Pygathrix bieti C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 03-Jun-2002 C;Accession: T17163 R;Wang, W.; Forstner, M.R.J.; Zhang, Y.P.; Lui, Z.M.; Wei, Y.; Huang, H.O.; Hu, H.G.; Xi Int. J. Primatol. 18, 305-320, 1997 A;Title: A phylogeny of Chinese leaf monkeys using mitochondrial ND3-ND4 gene sequences. A;Reference number: Z18709 A;Rocession: T17163 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-459 cWAN> A;Cross-references: EWBL: U92956; NID:g2290437; PID:g2290440; PIDN:AAD08823.1 C;Superfamily: NADH dehydrogense (ubiquinone) chain 4 C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation:	Alignment Scores: 0.0402 Length: 459 Score: 112.00 Matches: 80 Score: 36.54 Conservative: 72 Best Local Similarity: 19.23 Mismatches: 142 Query Match: 2 Gaps: 19 US-09-768-781-2 (1-1389) x T17163 (1-459)	Qy 142 TTTAGCATCCTTTTCTACACTGTGGGGGGGGCTGCATCTGTACATG 201	322 GATAAACGGTATCATTATTTATGCATCTAGAGACCTGTTATCAGATGTTTG 174		Db 221 ValGluAlaProlleAlaGLySerMetValLeuAlaAlaValLeuLeuLysLeuGlyGly 240 dy 679 TATGGGGCCACCCTTTGCAATATCTTGGCTATCAGATCAAGTACGAT 726	Oy 787 GAGATCACTTCCCGCCTCCTGATTCTGGTGCTCTTCTCAGCCACTTTGAAATTGAAGGCT 846 271 MetThrSerSerthrCysLeuArgGlnThrAspLeuLysSerLeulleAlaTyrSerSer 290

```
ologia, A.; Ecker, J.R.; Palm, C.J.; Federapiel, N.A.; Kaul, S.; White, O.; Alonso, C. W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; L. N.P.; Hughes, B.; Huizar, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; I. N.P.; Hughes, B.; Huizar, L.; Conway, A.R.; Creasy, T.H.; Dewar, L.; Edons, J.C.; Khan, S.; Khaykin, E.; Kim, C., Lio, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malti, R.; Marziali, L.; J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malti, R.; Marziali, M.; Rooney, T.; Rowley, D.; Sakano, H.

hors: Salzaberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

hors: Salzaberg, S.L.; Tasser, C.M.; Venter, J.C.; Davis, R.W.

hors: Salzaberg, S.L.; Tasser, C.M.; Venter, J.C.; Davis, R.W.

hors: Malti, MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cule type: DNA-
dues: 1-785 <STO>
is-references: GB:AE005172; NID:g4966359; PIDN:AAD34690.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------GGGCAGAACTGGGGACATATGGGCCTGCACTAT 1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         099 AGTGTGAGGTTGGTA---GAGAATGTGATCATGGTCTTGGTTTTTAAGTTCTTTGGAGTG 1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 AAAGTGTTACTGAATTACTGTCATTCCTTGATTGCCTTGCAGCTCATTATTGCTTATCTG 1215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 netical protein F309.18 - Arabidopsis thaliana
ises: Arabidopsis thaliana (mouse-ear cress)
s: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
ission: A86299
                                                                                                                                                                                                                          964 CTGGTGGTCCTGATT--------TCAGTCACCATCCTCTATGCTGGCATC 1005
                                                                                                                                                                                                                                                                                                                                            391
                                                                                                                                                              -----SerPheThrdjyAla 312
                                                                                                                                                                                                                                                                                                                                                                          333 AsnTyrGluArgThrHisSer---ArgIleMetLeuLeuSerArgGlyLeuGlnThrLeu 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||| :::::: ||| || 352 LeuProLeuMetAlaPheTrpPheAlaAlaAsnLeuThrAsnLeuAlaLeuProPro 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ::::::|||
392 ThrlleMetLeuThr--------GlyLeuAsnMetLeuIleThrAlaLeu 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |||::: :::||||||::
406 TyrSerLeu---TyrMetLeuValThrThrGlnArgGlyThrLeuThrSerHisllelle 424
847 GIGCCCTTCCTAGIGCICAACTTCCTGAICATCCTCTTTGAG---CCCTGGAITAAGTTC 903
                                                                                                        904 TGGAGAAGTGGTGCCCAGATGCCCAATAACATTGAGAAAAACTTCAGCCGGGTCGGCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          258 CCATTGCGCTCACTCTTCACC---CATAATGTAGTAGACTACCTCCAT 1302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             785
89
84
172
107
20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 768-781-2 (1-1389) x A86299 (1-785)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.0495
111.50
38.27%
19.69%
4.38%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity:
cal Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           us: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ent Scores:
                                                                                                                                                                 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                           990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11
```

ઠે

ò

a	30 Le	::::: LeuValPheSerGlnPhePheTyrLeuPheLeuLysProCysGlyGlnAlaGlyProVal 49
à	190	GCTTTGTACATGGTTAGAATCTATCGAAAGAATAGTGAA 228
ą	50 AL	aGlnIleLeuAlaGlyIleValLeuSerLeuLeuThrIleIleArgLy8ValHisGlu 69
ර සි	229 AC	ACTIACTGGATGACATACACTITICTTTTATGTTTTCATCCATTATGGTCCAGTTG 288 :::
}		, "
; a		AlaPheValPheLeuileGlyLeuGluileAspLeuAspPheMet 104
ò	346 CA	CATCTAATCCTCTTGGGACCTGTTATCAGATGTTTGGAGGCCATGATTAAGTACCTCACA 405
g G	105 Ly	BArgAsnLeuLysAssnSerileVallleThrLeuGlySerLeuVallleSerGlyIle 124
& 1		CTGTGGAAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGAAGA
a 8		
s 음	139	
Š	478	GAGGTGCTGATAGAATGGGAGGTGGCCACTCCATCCGGACC 519
g	159 AL	
ઠે	520 CT	GGCTATGCACCGCAATGCCTACAAACGTATGTCAACATCCAAGCCTTCCTGGGCTCA 579
ą	179 Le	:: LeualaileSerCysGlyLeuPheileGluileThrAsnile 192
È	580 GT	GTGCCCCAGCTGACCTATCAGCTTATGTGAGCCTGATCTCTGCAGAGGTTCCCCTGGGT 639
셤	193	PhelleTyrThr11eValLeuSerPhelleSerGlyThrMetThrAlaAsp 209
કે	640 AG	AGAGITGIGCIAAIGGIAITITCCCIGGIAICTGICACCIAIGGGGCCACCCIIIGCAAI 699
g G	210 11	ePheileTyrSerPheAlaThrGlyValileIleLeuThrAsnArgPheLeuAlaSer 229
È		ATGITGGCTATCCAGATCAAGATGACTACAAGATTCGCCTTGGGCCACTAGAA 756
g G	230 Tr	TrpleuProlysArgAsnProlysGlulysTyrLeuSerLysAlaGluThrLeuAlaPhe 249
हें ह		GTCCTCTGCATCACCATCTGGCGGACATTGGAGATCACTTCCCGCCTC 804
g ,		
දු ද	805 CT	CTGATTCTGGTGCTCTTCTCAGCCACTTTGAAATTG 840 ::: ::
ሯ		GGCTGTGCCCTTCCTAGTGCTCAACTTCCTGATCATCTTTGAGCCCCTGGATTAAG 900
a a	290 GI	::: ::: ::: ::: ::::::
ઠે	901 TT	CTGGAGAGTGGTGCCCAGATGCCCAATAACATTGAGAAAAACTTCAGCCGGGTGGC 960
QQ	11 310 PH	
ò	961 AC	ACTCTGGTGGTCCTGATTTCAGTCACCATCCTCTATGCTGGCATCAACTTCTTTGC 1017
g	326 Gl	yMetThrValAlaLeuSerLeuLeuGlyLysLeuLeuGlyValLeuPheAlaCysSer 345
ઠે	1018	
g	346 Ph	eLeuLyslleProLysGlnTyrTrpLeuPheLeuSerThrMetLeuSerValLys 364
ઠે	1054 CT	CTCGTCGACAAAGGGCAGAACTGGGGCATATGGGCCTGCACTATAGTGTGAGGTTGGTA 1113

```
MADRIZ dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 [similarity] - Pygathrix bieti mit C;Species: mitcohondrion Pygathrix bieti C;Species: mitcohondrion Pygathrix bieti C;Darcession: 19-May-2000 #sequence_revision 19-May-2000 #text_change 03-Jun-2002 C;Accession: T17166

R;Wang, W.; Forstner, M.R.J.; Zhang, Y.P.; Lui, Z.M.; Wei, Y.; Huang, H.Q.; Hu, H.G.; Xi Int. J Primatol. 18, 305-320, 1997

A;Fitle: A phylogeny of Chinese leaf monkeys using mitochondrial ND3-ND4 gene sequences. A;Reference number: Z18709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A/Status: preliminary
A/Molecule type: DNA
A/Redidues: 1-459 <WANN
A/Cross-references: EMBL:U92957; NID:g2290441; PID:g2290444; PIDN:AAD08826.1
C/Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C/Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
                               1114 GAGAATGTGATCATGGTCTTGGTTTTTAAGTTCTTTGGAGTGAAAGTGTTACTGAATTAC 1173
                                                                                            1174 TGTCATTCCTTGATTGCCTTGCAGCTCATTATTGCTTATCTGATTTCC-----ATTGGC 1227
                                                                                                                                                           1228 TTCATGCTCCTTTTCTTCCAG-----TACTTGCATCCATTGCGCTCACTCTTCACC 1278
                                                                386
                                                                                                                155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----ProLeuLeu 179
------ValLeuLeuAsp 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTTAGCATCCTTTTCTCCACCTTTTTGTACTGTGGGGAGGCTGCATCTGCTTTGTACATG 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        262 ATGITITCATCCATTATGGTCCAGTTGACCCTCATTTTTGTCCACAGAGATCTAGCCAAA 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .----- 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            202 GTTAGAATCTATCGAAAGAATAGTGAAACTTACTGGATGACATACACCTTTTCTTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              322 GATAAACCGCTATCATTATTATGCATCTAATCCTTGGGACCTGTTATCAGATGTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGGCCATGATTAAGTACCTCACACTGTGGAAGAAGAGGAGGAGGAGGAGCCCTATGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   442 AGCCTCACCCGAAAGAAGATGCTAATAGATGGCGAGGAGGTGCTGATAGAATGGGAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----ThrThrTrp-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCCACTCCATCCGGACCCTGGCTATGCACCGCAATGCCTACAAACGTATGTCACAGATC
                                                     374 SerAsh------LeuMetTyrLysLysTrpPheThrProValVal-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  459
80
72
1142
1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                          1279 CATAATGTAGTAGACTACCTCCATTGTGTCTGCTGT 1314
                                                                                                                                                                                                                                              ::: ||| ::: ||| 426 PheAspThrThrGluGluLeuArgValLeuThrCys 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-768-781-2 (1-1389) x T17166 (1-459)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.0501
111.00
36.54%
19.23%
4.36%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Accession: T17166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    502
 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177
                                                                                                                                                                                                                                                                                         RESULT 12
                                                                                                                                                                                                                                                                                                            T17166
NADH2 d
                                 ò
                                                              g
                                                                                       ò
                                                                                                                     g
                                                                                                                                                           ò
                                                                                                                                                                                       g
                                                                                                                                                                                                                       ठे
                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
```

embrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

		C: Keywords: me
ò	562 CAAGCCTTCCTGGGCTCAGTGCCCCAGCTGACCTATCAGCTCTATGTGAGCCTGATCTCT 621	
a	201 MetAlaPheMetValLysMetProLeuTyrGlyLeuHisLeuTrpLeuProLysAlaHis 220	Alignment Scor Pred. No.:
δ	622 GCAGAGAGGTTCCCCTGGGTAGAGTTCTGCTAATTTTTCCTATTTTTCCTAATTTTTCTCTAATTTTTCTCTCAATTTTTCTCTTAATTTTTT	Score:
; 셤	ValgluAlaProf1eAlaGlySerMetValLetAlaAlaAlaGlySerUGlyGly	Best Local Sim
ě		DB:
s		US-09-768-781-
ag	241 TyrGlyMetMetArgLeuThrSerIleLeuAanProLeuThrGluTyrMetAlaTyr 259	Ox 142 mmp8
ò	727 GACTACAAGATTCGCCTTGGGCCACTAGAAGTCCTCTGCCATCACCATCTGGCGGACATTG 786	7
ឧ		118
È	787 GAGATCACTICCCGCCTCCTGATTCTGGTGCTCTTCTCAGCCACTTTGAAATTGAAAGGCT 846	Oy 202 GITA
q	271 MetThrSerSerThrCysLeuArgGlnThrAspLeuLysSerLeuIleAlaTyrSerSer 290	Db 138 AenG
ò		Oy 262 ATGT
<u>a</u>	::: :::	Db 156
ઠે	TRABACAAGTIGCCCAGATIGCCCAAAAAAAAAAAAAAAAAAAA	Qy 322 GATA
) f		Db 174
È	ma************************************	Qy 382 GAGG
S	::: :::::	Db 177
අ	313 IleValLeuMetIleAlaHisGlyLeuThrSerSerMetLeuPheCysLeuAlaAsnSer 332	Ov 442 AGCC
ò	1006 AACTICICITGCIGGICAGCITIGCAGITIGGCAGACAGAGAICICGICGACAAA 1065	
a	333 AsnTyrGluArgThrHisSerArgIleMetLeuLeuSerArgGlyLeuGlnThrLeu 351	
È	1066	202
qq		
È	1099 AGTGTGAGGTTGGTAGAGAATGTGATCATGGTCTTGGTTTTTAAGTTCTTTGGAGTG 1155	
g		201
ò	1156 AAAGTGTTACTGAATTACTGTCATTCCTTGATTGCCTTGCAGCTCATTATTGCTTATCTG 1215	Qy 622 GCAG
g		Db 221 ValG
8		Oy 679 TATG
3 8	::::::::::::::::::::::::::::::::::::::	Db 241 TyrG
3 8	1960 CONTROLOGICA ATTACHORINATION TO THE CONTROL OF	Qy 727 GACT
S 6	4.2.5. Der Monte of the Control of t	Db 260
	A SOUTH THE TRANSPORT TO THE TRANSPORT T	Oy 787 GAGAT
T17172		Db 271 MetT
S'C	Applies weingliedenase (uniquimone) (br. 1.0.3.3) Chain 4 [SIMILIAILLY] - Fygarmix Dieti Miq C. Species Mitocondrion Pygathix bieti	Qy 847 GTGCC
טֿב <u>ּ</u>	C.bate: 19-may-2000 #sequence_revision 19-may-2000 #text_change 03-Jun-2002 C.Accession: T17172	 Db 291 ValSe

```
CTGGTGGTCCTGATT----------TCAGTCACCATCCTCTATGCTGGCATC 1005
                                                                                                                                                                                                                                                                                                                                                      155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200
                                                                                                                                                                                                                                                        TyrileLeuPheGluThrThrLeuIleProThrLeuIleIleIleThrArgTrpGly 137
                                                                                                                                                                                                                                                                                                          261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         270
                                                                                                                                                                                                                 AGCATCCTTTTCTCCACCTTTTTGTACTGTGGGGAGGCTGCATCTGCTTTGTACATG 201
                                                                                                                                                                                                                                                                                                                                                                                               ITITCATCCATTATGGTCCAGTTGACCCTCATTTTTGTCCACAGAGATCTAGCCAAA 321
                                                                                                                                                                                                                                                                                                                                                                                                                        ||||::: :::|||
---GlySerLeuProLeuLeuIleMetLeuLeuPheValHisAsnAsnLeuGlySer 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAACCGCTATCATTATTTATGCATCTAATCCTCTTGGGACCTGTTATCAGATGTTTG 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -------ProLeuLeu 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ceurhralaGlnLysLeu------ 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AlapheMetValLysMetProLeuTyrGlyLeuHisLeuTrpLeuProLysAlaHis 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGGTTCCCCTG---GGTAGAGTTGTGCTAATGGTATTTTCCCTGGTATCTGTCACC 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         313 IlevalLeuMetileAlaHisGlyLeuThrSerSerMetLeuPheCysLeuAlaAsnSer 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCTTCCTAGTGCTCAACTTCCTGATCATCCTCTTTGAG----CCCTGGATTAAGTTC 903
                                                                                                                                                                                                                                                                                                        :::
3InAlaGluArgLeuAsnAlaSerThrTyrPheLeuPheTyrThrLeuThr-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTCACCCGAAAGAAGATGCTAATAGATGGCGAGGAGGTGCTGATAGAATGGGAAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CACTCCATCCGGACCCTGGCTATGCACCGCAATGCCTACAAACGTATGTCACAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3GG------GCCACCCTTTGCAATATGTTGGCTATCCAGATCAAGTACGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |||
3]yMetMetArgLeuThrSerIleLeuAsnProLeuThrGluTyrMetAlaTyr---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TACAAGATTCGCCTTGGGCCACTAGAAGTCCTCTGCATCACCATCTGGCGGACATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||| ::::::|||
-------ProPheLeuMetLeuSerLeuTrpGlyMetIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----LeuAsnIle-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCCATGATTAAGTACCTCACACTGTGGAAGAAGAAGAGGAGGAGGAGGAGCCCTATGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCCTTCCTGGGCTCAGTGCCCCAGCTGACCTATCAGCTCTATGTGAGCCTGATCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATCACTŢĊÇCGCCTCÇŢĠATTCTGGTGCTCTTCTCAGCCACTTTGAAATTGAAGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGAGAAGTGGTGCCCAGATGCCCAATAACATTGAGAAAAACTTCAGCCGGGTCGGCACT
                    459
80
772
1142
1192
               Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HisAsnLeuThrTrpLeuAlaCys-----
                                                                                                                                                                    (1-1389) x T17172 (1-459)
               0.0501
111.00
36.54*
19.23*
                                                             larity:
imilarity:
res:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: T17172
R;Wang, W.; Forstner, M.R.J.; Zhang, Y.P.; Lui, Z.M.; Wei, Y.; Huang, H.Q.; Hu, H.G.; Xi
INt. J. Primatol. 18, 305-320, 1997
A;Accession: T1712
A;Accession: T1712
A;Status: preliminary
A;Status: preliminary
A;Status: DNA
A;Residues: 1-459 <WAN>
A;Cross-references: EMBL:U92959; NID:G2290449; PID:G2290452; PIDN:AAD08832.1
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4
```

### ##################################	Db 180 ThrLeuthralaGlnLysLeu
125 Canada Describer Control of State Control of Species: mitochondrion Pygathrix bieti 5pecies: mitochondrion Pygathrix bieti 5pecies: mitochondrion Pygathrix bieti 5pecies: mitochondrion Pygathrix bieti 6pecies: mitochon of State Control of State Control of State Control of Chinese Leaf monkeys using mitochon Reference number: 218709 6ccession: T17169 6cc	Qy 787 GAGATCACTTCCGCCTCTGATTCTGGTGCTCTTCTCAGCCACTTTGAAATTGAAGGCT 846 271 MetTh:SerSerThrCysLeuArgGlnThrAspLeuLysSerLeuIleAlaTyrSerSer 290 271 MetTh:SerSerThrCysLeuArgGlnThrAspLeuLysSerLeuIleAlaTyrSerSer 290 Qy 847 GTGCCCTTCCTAGTGCTCCATTCCTGATCATCTTTGAGCCTGGATTAAGTTC 903 291 ValSerHisMetAlaLeuValIleMetAlaSerLeuIleGlnThrPrOTTp 307 Qy 904 TGGAGAAGTGGTGCCCAATAACATTGAGAAAACTTCAGCGGGTCGGCACT 963 Db 308
Alignment Scores: Pred. No.: Pred. No.: 10.50 Matches: Score: Score: 110.50 Matches: 86 Percent Similarity: 36.45\$ Conservative: 70 Best Local Similarity: 20.09\$ Mismatches: 126 DB: 2.09-768-781-2 (1-1389) x T17169 (1-459) Oy 142 TTTAGCATCCTTTTCTCCACCTTTTGTACTGTGGGGAGGCTGCATCTGCTTTGTACATG 201	1066
	1216 ATTTCCATTGCTTCATTCTTCAGTACTTGCATCATTGCTCCTTGCTCCATTGCTTCCAGTACTTGCATCATTGCTTCCAGTACTTGCATCATTGCTTCCAGTACTTGCATCATTGCTTGCTTGCTTGCTTGCTTGCTTGCTTG
Db 174	RESULT 15 B97305 probable cation efflux pump (multidrug resistance protein) [imported] - Clostridium acet Cypedes: Clostridium acetobutylicum (;pecies: Clostridium acetobutylicum (;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 C;Accession: B97305 R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,

0 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	alPhe ccar	Search completed: April 1, 2003, 08:59:15 Job time : 63.5 secs					
Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. Bacteriol. 183, 4823-4838, 2001 Ittle: Genome Sequence and Comparative Analysis of the Solvent-Produc Reference number: A96900; MUD:21359325, PMID:21359325 Status: prellminary Molecule type: DNA Residues: 1-461 -KUR> Cross-references: GB-AE001437; PIDN:AAK81229.1; PID:g15026374; GSPDB:Experimental source: Clostridium acetobutylicum ATCG824 Genetics: 0.0697 Length: 461 Gene: CA03295 ignent Scores: 0.0697 Length: 81 conservative: 75 realt Similarity: 20.254 Mismatches: 137 ery Match: 109-70 Mismatches: 107 conservative: 75 ery Match: 107 20.09-768-781-2 (1-1389) x B97305 (1-461)	Qy 238 ATGACATACACCTTTTCTTTCTTTTTTGTTTTCATCATTGTCCCTC 294 1::::::::::::::::::::::::::::::::::::	Qy 346 CATCTAATCCTTGGGACCTGTTATCAGATGACGCCATGATTAAGTACCTCACA 405 b 1::	Qy 466 ATAGATGGCGAG	Qy 541 TACAAACGTATGTCACAGACCTTCCTGGGCTCAGTCCCCAGCTGACCTAT 597 b ::: ::: :: c ::: ::: c	<pre>Qy 628 GTTCCCCTGGGTAGAGTTGTGCTAATTGCTGGTATCTGTCACCTATGGGCCC 687 ::: ::: ::: Db 239 IleIleArgGluIleValLeuValGlyPheSerThrPheIleIleGluIleAlaAsp 257 Qy 688 ACCTTTGCAATATGTTGGCTATCCAGATCAAGTACGATGACTACAAG 735 Db 258 AlaValValSerAlaValLeuAshAshValLeuTyrAlaGlyGlyAspSerAlaIle 277</pre>	ATTCGCCTTGGGCCACTAGAAGTCCTCTGCATCACCATCTGGCGGACATTGGAGATC	Oy 793 ACTTCCGGCTCTGATTCTGGTGCTCTTCTCA